

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 9, 2006, 21:57:27 ; Search time 9811 Seconds
 (without alignments)
 10989.232 Million cell updates/sec

Title: US-08-906-365-1

Perfect score: 1686

Sequence: 1 cagccattatacttgccac.....agaacccacagtctcagtga 1686

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : GenEmbl:
 1: gb_env:
 2: gb_pat:
 3: gb_ph:
 4: gb_pl:
 5: gb_pr:
 6: gb_ro:
 7: gb_sts:
 8: gb_sy:
 9: gb_un:
 10: gb_vi:
 11: gb_ov:
 12: gb_htg:
 13: gb_in:
 14: gb_om:
 15: gb_ba:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	1684.4	99.9	1740	2	BD093391	BD093391 Method fo
2	1684.4	99.9	1740	5	AB006590	AB006590 Homo sapi
3	1683.4	99.8	2011	2	AR606192	AR606192 Sequence
4	1683.4	99.8	2011	2	AX234658	AX234658 Sequence
5	1683.4	99.8	2011	2	AX676912	AX676912 Sequence
6	1683.4	99.8	2011	5	AF051427	AF051427 Homo sapi
7	1667.4	98.9	1898	2	A65127	A65127 Sequence 24

8	1667.4	98.9	1898	2	AR454163	AR454163 Sequence	
9	1667.4	98.9	1898	2	AR490594	AR490594 Sequence	
10	1667.4	98.9	1898	2	AX323078	AX323078 Sequence	
11	1637.4	97.1	2433	2	BD170497	BD170497 Fluoresce	
12	1634	96.9	1647	2	BD091391	BD091391 Estrogen	
13	1634	96.9	1647	2	AR233984	AR233984 Sequence	
14	1634	96.9	1647	2	AR316860	AR316860 Sequence	
15	1634	96.9	1647	2	AX029400	AX029400 Sequence	
16	1609.4	95.5	1660	2	AX592833	AX592833 Sequence	
c	17	1609.4	95.5	1660	2	AX592834	AX592834 Sequence
	18	1496.4	88.8	2041	5	AF051428	AF051428 Homo sapi
	19	1496.4	88.8	2745	5	AF060555	AF060555 Homo sapi
	20	1495.8	88.7	3593	5	AB006589	AB006589 Homo sapi
	21	1485.6	88.1	1651	5	CJERB	Y09372 C.jacchus m
	22	1453.6	86.2	1460	2	A61586	A61586 Sequence 4
	23	1453.6	86.2	1460	2	AR075921	AR075921 Sequence
	24	1453.6	86.2	1460	2	BD131061	BD131061 Orphan re
	25	1453.6	86.2	1460	2	AX022458	AX022458 Sequence
	26	1450.4	86.0	1460	2	BD078109	BD078109 Discrimin
	27	1450	86.0	1560	5	HSRNAERB	X99101 H.sapiens m
	28	1434	85.1	1434	2	A65104	A65104 Sequence 1
	29	1434	85.1	1434	2	AR454145	AR454145 Sequence
	30	1434	85.1	1434	2	AR490576	AR490576 Sequence
	31	1434	85.1	1434	2	AX323055	AX323055 Sequence
	32	1405.2	83.3	5554	5	AB209620	AB209620 Homo sapi
	33	1374.2	81.5	1640	5	AF393815	AF393815 Macaca ar
	34	1306.6	77.5	1566	5	AF393816	AF393816 Callithri
	35	1256.6	74.5	1611	14	AF110402	AF110402 Bos tauru
	36	1254.6	74.4	1584	14	AF177936	AF177936 Ovis arie
	37	1247.2	74.0	2344	6	AB190769	AB190769 Rattus no
	38	1247	74.0	1251	2	A65105	A65105 Sequence 2
	39	1247	74.0	1251	2	AR454146	AR454146 Sequence
	40	1247	74.0	1251	2	AR490577	AR490577 Sequence
	41	1247	74.0	1251	2	AX323056	AX323056 Sequence
	42	1247	74.0	1257	2	A65123	A65123 Sequence 20
	43	1247	74.0	1257	2	AR454160	AR454160 Sequence
	44	1247	74.0	1257	2	AR490591	AR490591 Sequence
	45	1247	74.0	1257	2	AX323074	AX323074 Sequence

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OM nucleic - nucleic search, using sw model

Run on: August 10, 2006, 00:28:57 ; Search time 341 Seconds
 (without alignments)
 9251.289 Million cell updates/sec

Title: US-08-906-365-1
 Perfect score: 1686
 Sequence: 1 cagccattatacttgcac.....agaacccacagtctcagtga 1686

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_NA:*

1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*

10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result		Query				
No.	Score	Match	Length	DB	ID	Description
<hr/>						
1	1684.4	99.9	1745	3	US-09-949-016-1563	Sequence 1563, Appl
2	1683.4	99.8	2011	3	US-09-768-185A-2	Sequence 2, Appl
3	1667.4	98.9	1898	3	US-09-608-088-24	Sequence 24, Appl
4	1667.4	98.9	1898	3	US-09-711-288-24	Sequence 24, Appl
5	1634	96.9	1647	3	US-09-139-617-2	Sequence 2, Appl
6	1634	96.9	1647	3	US-09-561-741A-2	Sequence 2, Appl
7	1634	96.9	1647	3	US-09-558-795-2	Sequence 2, Appl
8	1453.6	86.2	1460	2	US-08-836-620A-4	Sequence 4, Appl
9	1434	85.1	1434	3	US-09-608-088-1	Sequence 1, Appl
10	1434	85.1	1434	3	US-09-711-288-1	Sequence 1, Appl
11	1247	74.0	1251	3	US-09-608-088-2	Sequence 2, Appl
12	1247	74.0	1251	3	US-09-711-288-2	Sequence 2, Appl

13	1247	74.0	1257	3	US-09-608-088-20	Sequence 20, Appl
14	1247	74.0	1257	3	US-09-711-288-20	Sequence 20, Appl
15	1233.6	73.2	2568	2	US-08-836-620A-1	Sequence 1, Appli
16	1099.6	65.2	1458	2	US-08-836-620A-6	Sequence 6, Appli
17	453.4	26.9	68452	3	US-09-949-016-13305	Sequence 13305, A
18	453.4	26.9	325791	3	US-09-768-185A-1	Sequence 1, Appli
19	395.8	23.5	2764	3	US-09-893-666A-1	Sequence 1, Appli
20	390.8	23.2	4963	2	US-08-076-726-16	Sequence 16, Appl
21	390.8	23.2	4963	2	US-08-260-452-9	Sequence 9, Appli
22	390.8	23.2	4963	2	US-08-481-970-9	Sequence 9, Appli
23	390.8	23.2	4963	2	US-08-897-719-9	Sequence 9, Appli
24	390.8	23.2	4963	3	US-09-163-269-9	Sequence 9, Appli
25	390.8	23.2	4963	3	US-09-281-674-9	Sequence 9, Appli
26	390.8	23.2	4963	3	US-09-777-317B-9	Sequence 9, Appli
27	389.2	23.1	2092	3	US-10-052-092-6	Sequence 6, Appli
28	389.2	23.1	6450	3	US-09-041-886-34	Sequence 34, Appl
29	389.2	23.1	6450	3	US-08-453-998-1	Sequence 1, Appli
30	389.2	23.1	6450	3	US-10-027-983-3	Sequence 3, Appli
31	389.2	23.1	6450	3	US-09-949-016-18	Sequence 18, Appli
32	389.2	23.1	6450	3	US-10-052-092-1	Sequence 1, Appli
33	389.2	23.1	6450	3	US-10-052-092-7	Sequence 7, Appli
34	389.2	23.1	6450	3	US-10-081-563-1	Sequence 1, Appli
35	389.2	23.1	6610	3	US-10-052-092-20	Sequence 20, Appl
36	388	23.0	1788	3	US-10-052-092-24	Sequence 24, Appl
37	366.2	21.7	1978	3	US-10-052-092-23	Sequence 23, Appl
38	326.6	19.4	2106	3	US-10-052-092-5	Sequence 5, Appli
39	312.4	18.5	8566	3	US-10-027-983-10	Sequence 10, Appl
40	296.4	17.6	2495	3	US-09-771-357-104	Sequence 104, App
41	296.4	17.6	2495	3	US-10-059-579A-104	Sequence 104, App
42	287.2	17.0	1218	3	US-10-027-983-98	Sequence 98, Appl
43	285.6	16.9	1644	3	US-10-052-092-2	Sequence 2, Appli
44	285.6	16.9	1956	3	US-08-693-940-2	Sequence 2, Appli
45	285.6	16.9	1956	3	US-09-566-660-2	Sequence 2, Appli

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OM nucleic - nucleic search, using sw model

Run on: August 10, 2006, 00:59:46 ; Search time 2247 Seconds
 (without alignments)
 9219.828 Million cell updates/sec

Title: US-08-906-365-1

Perfect score: 1686

Sequence: 1 cagccattatacttgcccac.....agaacccacagtctcagtga 1686

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000.

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA_Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*

10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*

12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*

13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*

14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*

15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*

16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
<hr/>						
1	1686	100.0	1686	9	US-10-745-379-1	Sequence 1, Appli
2	1686	100.0	1686	16	US-11-026-800-1	Sequence 1, Appli
3	1684.4	99.9	1740	3	US-09-815-068A-1	Sequence 1, Appli
4	1684.4	99.9	1740	6	US-10-198-785-1	Sequence 1, Appli
5	1683.4	99.8	2011	4	US-09-768-185A-2	Sequence 2, Appli
6	1683.4	99.8	2011	6	US-10-157-031-105	Sequence 105, App

7	1683.4	99.8	2011	7	US-10-392-274-3	Sequence 3, Appli
8	1683.4	99.8	2011	10	US-10-888-313A-101	Sequence 101, App
9	1683.4	99.8	6777	7	US-10-376-566-10	Sequence 10, Appl
10	1637.4	97.1	2433	8	US-10-460-845-1	Sequence 1, Appli
11	1496.4	88.8	2041	10	US-10-756-149-1507	Sequence 1507, Ap
12	1496.4	88.8	2745	11	US-10-826-585-22	Sequence 22, Appl
13	1495.8	88.7	3593	7	US-10-376-566-3	Sequence 3, Appli
14	1453.6	86.2	1460	6	US-10-278-481-4	Sequence 4, Appli
15	1433.8	85.0	1682	7	US-10-373-271-2	Sequence 2, Appli
16	1236.4	73.3	2555	16	US-11-136-527-2114	Sequence 2114, Ap
17	1233.6	73.2	2568	6	US-10-278-481-1	Sequence 1, Appli
18	1167.4	69.2	1427	7	US-10-376-566-15	Sequence 15, Appl
19	1099.6	65.2	1458	6	US-10-278-481-6	Sequence 6, Appli
20	1056.4	62.7	1512	16	US-11-136-527-3577	Sequence 3577, Ap
21	865	51.3	1215	7	US-10-376-566-14	Sequence 14, Appl
22	600	35.6	600	13	US-11-060-756-2172	Sequence 2172, Ap
23	600	35.6	600	13	US-11-060-756-2173	Sequence 2173, Ap
24	600	35.6	600	13	US-11-060-756-6444	Sequence 6444, Ap
25	600	35.6	600	13	US-11-060-756-6445	Sequence 6445, Ap
26	453.4	26.9	113000	7	US-10-376-566-16	Sequence 16, Appl
27	453.4	26.9	325791	4	US-09-768-185A-1	Sequence 1, Appli
28	452.4	26.8	597	3	US-09-864-761-7903	Sequence 7903, Ap
29	433.8	25.7	2384	8	US-10-663-561-148	Sequence 148, App
30	415.8	24.7	2188	8	US-10-663-561-147	Sequence 147, App
31	396.8	23.5	600	16	US-11-136-527-7673	Sequence 7673, Ap
32	395.8	23.5	2764	3	US-09-893-666A-1	Sequence 1, Appli
33	391.2	23.2	2043	8	US-10-663-561-146	Sequence 146, App
34	390.8	23.2	1788	3	US-09-853-033-1	Sequence 1, Appli
35	390.8	23.2	4963	3	US-09-281-674-9	Sequence 9, Appli
36	390.8	23.2	4963	3	US-09-777-317-9	Sequence 9, Appli
37	390.8	23.2	4963	3	US-09-892-227-9	Sequence 9, Appli
38	389.2	23.1	1785	7	US-10-095-373A-1	Sequence 1, Appli
39	389.2	23.1	1793	13	US-11-035-623-1	Sequence 1, Appli
40	389.2	23.1	1809	13	US-11-035-623-11	Sequence 11, Appl
41	389.2	23.1	2092	3	US-09-952-680A-9	Sequence 9, Appli
42	389.2	23.1	2092	6	US-10-052-092-6	Sequence 6, Appli
43	389.2	23.1	2092	7	US-10-157-899A-54	Sequence 54, Appl
44	389.2	23.1	2092	7	US-10-437-107-6	Sequence 6, Appli
45	389.2	23.1	2092	9	US-10-215-982-9	Sequence 9, Appli

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OM nucleic - nucleic search, using sw model

Run on: August 10, 2006, 03:22:02 ; Search time 563 Seconds
 (without alignments)
 4755.765 Million cell updates/sec

Title: US-08-906-365-1

Perfect score: 1686

Sequence: 1 cagccattatacttgcccac.....agaacccacagtctcagtga 1686

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 2200221 seqs, 794037843 residues

Total number of hits satisfying chosen parameters: 4400442

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_NA_New:*

1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*

9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*

10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
<hr/>						
1	1683.4	99.8	2011	8	US-11-283-329-93	Sequence 93, Appl
2	1683.4	99.8	2011	9	US-11-346-759-101	Sequence 101, App
3	1000	59.3	1000	8	US-11-266-748A-395231	Sequence 395231,
C	4	1000	59.3	1000	8	Sequence 466277,
	5	450.4	26.7	2186	6	Sequence 24, Appl
	6	389.8	23.1	1824	6	Sequence 5, Appli
	7	389.8	23.1	3499	6	Sequence 2, Appli
	8	389.2	23.1	6450	8	Sequence 120, App
	9	389.2	23.1	6450	8	Sequence 91, Appl
	10	389.2	23.1	6450	9	Sequence 100, App
	11	352.8	20.9	963	6	Sequence 25, Appl
	12	319.2	18.9	996	6	Sequence 3, Appli

13	179.6	10.7	611	8	US-11-266-748A-214650	Sequence 214650,
c 14	130	7.7	3540	8	US-11-266-748A-71864	Sequence 71864, A
c 15	130	7.7	3540	8	US-11-266-748A-106889	Sequence 106889,
16	130	7.7	3540	8	US-11-266-748A-124675	Sequence 124675,
17	129	7.7	1566	6	US-10-526-940-2	Sequence 2, Appli
18	129	7.7	2221	8	US-11-283-329-95	Sequence 95, Appli
19	129	7.7	2402	8	US-11-266-748A-32133	Sequence 32133, A
20	113.8	6.7	1377	6	US-10-526-940-1	Sequence 1, Appli
21	113.8	6.7	5216	6	US-10-507-700-5	Sequence 5, Appli
22	113.8	6.7	5253	8	US-11-283-329-99	Sequence 99, Appli
23	112.2	6.7	1503	6	US-10-526-940-7	Sequence 7, Appli
24	110.6	6.6	2193	8	US-11-283-329-97	Sequence 97, Appli
25	105.8	6.3	5221	6	US-10-507-700-3	Sequence 3, Appli
26	95.2	5.6	3514	6	US-10-523-899-4	Sequence 4, Appli
27	95.2	5.6	3768	6	US-10-523-899-1	Sequence 1, Appli
28	95.2	5.6	4314	8	US-11-283-329-107	Sequence 107, App
29	89.6	5.3	2575	9	US-11-207-382-11	Sequence 11, Appli
30	88.6	5.3	2263	8	US-11-266-748A-185290	Sequence 185290,
31	88.6	5.3	2263	8	US-11-266-748A-192812	Sequence 192812,
32	88.6	5.3	2481	8	US-11-266-748A-59173	Sequence 59173, A
33	88.6	5.3	2549	8	US-11-283-329-111	Sequence 111, App
34	88.6	5.3	2699	8	US-11-283-329-109	Sequence 109, App
c 35	88.4	5.2	1442	8	US-11-266-748A-227525	Sequence 227525,
36	88.4	5.2	1442	8	US-11-266-748A-241597	Sequence 241597,
37	88.2	5.2	1855	8	US-11-266-748A-27269	Sequence 27269, A
38	88.2	5.2	2202	8	US-11-283-329-75	Sequence 75, Appli
39	88	5.2	1000	8	US-11-266-748A-391580	Sequence 391580,
c 40	88	5.2	1000	8	US-11-266-748A-482298	Sequence 482298,
c 41	86.4	5.1	788	8	US-11-266-748A-255985	Sequence 255985,
42	86.4	5.1	788	8	US-11-266-748A-316502	Sequence 316502,
43	86.4	5.1	3791	8	US-11-266-748A-32110	Sequence 32110, A
44	86.4	5.1	3791	9	US-11-207-382-26	Sequence 26, Appli
45	86.4	5.1	4788	8	US-11-283-329-101	Sequence 101, App

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 9, 2006, 22:16:02 ; Search time 8466 Seconds
 (without alignments)
 11136.309 Million cell updates/sec

Title: US-08-906-365-1

Perfect score: 1686

Sequence: 1 cagccattatacttgcccac.....agaacccacagtctcagtga 1686

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST:*

1: gb_est1:*

2: gb_est3:*

3: gb_est4:*

4: gb_est5:*

5: gb_est6:*

6: gb_htc:*

7: gb_est2:*

8: gb_est7:*

9: gb_est8:*

10: gb_est9:*

11: gb_gss1:*

12: gb_gss2:*

13: gb_gss3:*

14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	1168.4	69.3	2712	6	AK054290	AK054290 Mus muscu
2	1168.4	69.3	3363	6	AK054413	AK054413 Mus muscu
3	962	57.1	3144	6	AK054301	AK054301 Mus muscu
4	584.4	34.7	587	8	CV024245	CV024245 1485 Full
5	500.8	29.7	727	2	BG722442	BG722442 602693671
6	403.4	23.9	621	9	DB025815	DB025815 DB025815
7	364.6	21.6	4248	6	AK041525	AK041525 Mus muscu
8	364.6	21.6	4321	6	AK036627	AK036627 Mus muscu

9	353.8	21.0	570	9	DB052117	DB052117	DB052117
10	353.6	21.0	2591	6	AK077236	AK077236	Mus muscu
11	353.4	21.0	572	9	DB029843	DB029843	DB029843
c 12	288.2	17.1	835	13	CW720839	CW720839	MARC_1130
13	286.8	17.0	5439	6	HSM807087	BX640939	Homo sapi
14	278	16.5	4315	6	AK087638	AK087638	Mus muscu
15	276.6	16.4	703	4	BY720348	BY720348	BY720348
16	276.6	16.4	873	8	CO808332	CO808332	AGENCOURT
17	275.2	16.3	675	5	CF913882	CF913882	B0955G07-
c 18	260	15.4	810	13	CW720841	CW720841	MARC_1130
19	238.6	14.2	375	5	CJ075881	CJ075881	CJ075881
20	237.8	14.1	387	9	DR000137	DR000137	TC119215
21	220.2	13.1	663	4	BY720287	BY720287	BY720287
22	220	13.0	814	13	CW720570	CW720570	MARC_1129
23	219.6	13.0	1020	6	AK136228	AK136228	Mus muscu
24	215.8	12.8	735	12	BZ834605	BZ834605	CH240_209
c 25	214	12.7	1160	5	CD508522	CD508522	CDA91-C11
c 26	208	12.3	627	3	BM942391	BM942391	UI-M-BH3-
27	201.2	11.9	2735	6	AK054182	AK054182	Mus muscu
28	196.4	11.6	652	7	BB666338	BB666338	BB666338
29	189.4	11.2	623	9	DN424563	DN424563	LIB4216-1
30	185.4	11.0	666	7	BB609187	BB609187	BB609187
31	184.6	10.9	627	7	BB666608	BB666608	BB666608
32	179.6	10.7	611	4	BX489897	BX489897	DKFZp686N
33	174.2	10.3	766	13	CW720571	CW720571	MARC_1129
c 34	173.4	10.3	531	1	AA224131	AA224131	zr14e02.r
35	169.8	10.1	1419	10	DT949269	DT949269	CFW102-E0
c 36	162.4	9.6	528	3	BM933826	BM933826	UI-M-BH3-
37	162.2	9.6	580	2	BG738138	BG738138	fp04f05.y
38	157.2	9.3	936	14	DQ038302	DQ038302	Pan trogl
39	157	9.3	642	7	BF058527	BF058527	7k31h08.x
40	157	9.3	782	7	AW134052	AW134052	fi14h07.y
41	157	9.3	1017	14	DQ038301	DQ038301	Homo sapi
42	155.6	9.2	877	10	DT235626	DT235626	JGI_CAAAT8
43	155.4	9.2	641	7	AW976636	AW976636	EST388745
44	155	9.2	650	5	CD594261	CD594261	RK090A3F1
45	155	9.2	650	5	CD594319	CD594319	RK090A4F1